



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/608,890
Source: 1690
Date Processed by STIC: 11/26/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202**

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/608,890

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 ✓ Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 ✓ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



1600

RAW SEQUENCE LISTING

DATE: 11/26/2004

PATENT APPLICATION: US/09/608,890

TIME: 09:49:26

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\11262004\I608890.raw

3 <110> APPLICANT: Johnson, Gary L.
 5 <120> TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To
 External
 6 Signals
 8 <130> FILE REFERENCE: CPI-004DVCP3CN
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/608,890
 C--> 11 <141> CURRENT FILING DATE: 2000-06-30
 13 <150> PRIOR APPLICATION NUMBER: 09/608,890
 W--> 14 <151> PRIOR FILING DATE: 2000-30-06 2000-06-30 ✓ replace with
 16 <150> PRIOR APPLICATION NUMBER: 08/440,421
 17 <151> PRIOR FILING DATE: 1995-05-15
 19 <150> PRIOR APPLICATION NUMBER: 08/323,460
 20 <151> PRIOR FILING DATE: 1994-10-14
 22 <150> PRIOR APPLICATION NUMBER: 08/049,254
 23 <151> PRIOR FILING DATE: 1993-04-15
 25 <150> PRIOR APPLICATION NUMBER: 08/410,602
 26 <151> PRIOR FILING DATE: 1995-03-24
 28 <150> PRIOR APPLICATION NUMBER: 08/472,934
 29 <151> PRIOR FILING DATE: 1995-06-06
 31 <160> NUMBER OF SEQ ID NOS: 27
 33 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply
 Corrected Diskette Needed

pp1-16

ERRORED SEQUENCES

2997 <210> SEQ ID NO: 14
 2998 <211> LENGTH: 1597
 2999 <212> TYPE: PRT
 3000 <213> ORGANISM: Mus musculus
 3002 <400> SEQUENCE: 14
 3003 Met Arg Asp Ala Ile Ala Glu Pro Val Pro Pro Pro Ala Leu Ala Asp
 3004 1 5 10 15
 3006 Thr Pro Ala Ala Ala Met Glu Glu Leu Arg Pro Ala Pro Pro Gln
 3007 20 25 30
 3009 Pro Glu Pro Asp Pro Glu Cys Cys Pro Ala Ala Arg Gln Glu Cys Met
 3010 35 40 45
 3012 Leu Gly Glu Ser Ala Arg Lys Ser Met Glu Ser Asp Pro Glu Asp Phe
 3013 50 55 60
 3015 Ser Asp Glu Thr Asn Thr Glu Thr Leu Tyr Gly Thr Ser Pro Pro Ser
 3016 65 70 75 80
 3018 Thr Pro Arg Gln Met Lys Arg Leu Ser Ala Lys His Gln Arg Asn Ser
 3019 85 90 95
 3021 Ala Gly Arg Pro Ala Ser Arg Ser Asn Leu Lys Glu Lys Met Asn Thr
 3022 100 105 110

pp 4-5

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Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\11262004\I608890.raw

```

3024 Pro Ser Gln Ser Pro His Lys Asp Leu Gly Lys Gly Val Glu Thr Val
3025      115      120      125
3027 Glu Glu Tyr Ser Tyr Lys Gln Glu Lys Lys Ile Arg Ala Thr Leu Arg
3028      130      135      140
3030 Thr Thr Glu Arg Asp His Lys Lys Asn Ala Gln Cys Ser Phe Met Leu
3031 145      150      155      160
3033 Asp Ser Val Ala Gly Ser Leu Pro Lys Lys Ser Ile Pro Asp Val Asp
3034      165      170      175
3036 Leu Asn Lys Pro Tyr Leu Ser Leu Gly Cys Ser Asn Ala Lys Leu Pro
3037      180      185      190
3039 Val Ser Met Pro Met Pro Ile Ala Arg Thr Ala Arg Gln Thr Ser Arg
3040      195      200      205
3042 Thr Asp Cys Pro Ala Asp Arg Leu Lys Phe Phe Glu Thr Leu Arg Leu
3043      210      215      220
3045 Leu Leu Lys Leu Thr Ser Val Ser Lys Lys Lys Asp Arg Glu Gln Arg
3046 225      230      235      240
3048 Gly Gln Glu Asn Thr Ala Ala Phe Trp Phe Asn Arg Ser Asn Glu Leu
3049      245      250      255
3051 Ile Trp Leu Glu Leu Gln Ala Trp His Ala Gly Arg Thr Ile Asn Asp
3052      260      265      270
3054 Gln Asp Leu Phe Leu Tyr Thr Ala Arg Gln Ala Ile Pro Asp Ile Ile
3055      275      280      285
3057 Asn Glu Ile Leu Thr Phe Lys Val Asn Tyr Gly Ser Ile Ala Phe Ser
3058      290      295      300
3060 Ser Asn Gly Ala Gly Phe Asn Gly Pro Leu Val Glu Gly Gln Cys Arg
3061 305      310      315      320
3063 Thr Pro Gln Glu Thr Asn Arg Val Gly Cys Ser Ser Tyr His Glu His
3064      325      330      335
3066 Leu Gln Arg Gln Arg Val Ser Phe Glu Gln Val Lys Arg Ile Met Glu
3067      340      345      350
3069 Leu Leu Glu Tyr Met Glu Ala Leu Tyr Pro Ser Leu Gln Ala Leu Gln
3070      355      360      365
3072 Lys Asp Tyr Glu Arg Tyr Ala Ala Lys Asp Phe Glu Asp Arg Val Gln
3073      370      375      380
3075 Ala Leu Cys Leu Trp Leu Asn Ile Thr Lys Asp Leu Asn Gln Lys Leu
3076 385      390      395      400
3078 Arg Ile Met Gly Thr Val Leu Gly Ile Lys Asn Leu Ser Asp Ile Gly
3079      405      410      415
3081 Trp Pro Val Phe Glu Ile Pro Ser Pro Arg Pro Ser Lys Gly Tyr Glu
3082      420      425      430
3084 Pro Glu Asp Glu Val Glu Asp Thr Glu Val Glu Leu Arg Glu Leu Glu
3085      435      440      445
3087 Ser Gly Thr Glu Glu Ser Asp Glu Glu Pro Thr Pro Ser Pro Arg Val
3088      450      455      460
3090 Pro Glu Leu Arg Leu Ser Thr Asp Thr Ile Leu Asp Ser Arg Ser Gln
3091 465      470      475      480
3093 Gly Cys Val Ser Arg Lys Leu Glu Arg Leu Glu Ser Glu Glu Asp Ser
3094      485      490      495
3096 Ile Gly Trp Gly Thr Ala Asp Cys Gly Pro Glu Ala Ser Arg His Cys

```

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Input Set : A:\pto.lm.txt

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```

3097          500          505          510
3099 Leu Thr Ser Ile Tyr Arg Pro Phe Val Asp Lys Ala Leu Lys Gln Met
3100          515          520          525
3102 Gly Leu Arg Lys Leu Ile Leu Arg Leu His Lys Leu Met Asn Gly Ser
3103          530          535          540
3105 Leu Gln Arg Ala Arg Val Ala Leu Val Lys Asp Asp Arg Pro Val Glu
3106 545          550          555          560
3108 Phe Ser Asp Phe Pro Gly Pro Met Trp Gly Ser Asp Tyr Val Gln Leu
3109          565          570          575
3111 Ser Gly Thr Pro Pro Ser Ser Glu Gln Lys Cys Ser Ala Val Ser Trp
3112          580          585          590
3114 Glu Glu Leu Arg Ala Met Asp Leu Pro Ser Phe Glu Pro Ala Phe Leu
3115          595          600          605
3117 Val Leu Cys Arg Val Leu Leu Asn Val Ile His Glu Cys Leu Lys Leu
3118 610          615          620
3120 Arg Leu Glu Gln Arg Pro Ala Gly Glu Pro Ser Leu Leu Ser Ile Lys
3121 625          630          635          640
3123 Gln Leu Val Arg Glu Cys Lys Glu Val Leu Lys Gly Gly Leu Leu Met
3124          645          650          655
3126 Lys Gln Tyr Tyr Gln Phe Met Leu Gln Glu Val Leu Gly Gly Leu Glu
3127          660          665          670
3129 Lys Thr Asp Cys Asn Met Asp Ala Phe Glu Glu Asp Leu Gln Lys Met
3130          675          680          685
3132 Leu Met Val Tyr Phe Asp Tyr Met Arg Ser Trp Ile Gln Met Leu Gln
3133 690          695          700
3135 Gln Leu Pro Gln Ala Ser His Ser Leu Lys Asn Leu Leu Glu Glu Glu
3136 705          710          715          720
3138 Trp Asn Phe Thr Lys Glu Ile Thr His Tyr Ile Arg Gly Gly Glu Ala
3139          725          730          735
3141 Gln Ala Gly Lys Leu Phe Cys Asp Ile Ala Gly Met Leu Leu Lys Ser
3142          740          745          750
3144 Thr Gly Ser Phe Leu Glu Ser Gly Leu Gln Glu Ser Cys Ala Glu Leu
3145          755          760          765
3147 Trp Thr Ser Ala Asp Asp Asn Gly Ala Ala Asp Glu Leu Arg Arg Ser
3148 770          775          780
3150 Val Ile Glu Ile Ser Arg Ala Leu Lys Glu Leu Phe His Glu Ala Arg
3151 785          790          795          800
3153 Glu Arg Ala Ser Lys Ala Leu Gly Phe Ala Lys Met Leu Arg Lys Asp
3154          805          810          815
3156 Leu Glu Ile Ala Ala Glu Phe Val Leu Ser Ala Ser Ala Arg Glu Leu
3157          820          825          830
3159 Leu Asp Ala Leu Lys Ala Lys Gln Tyr Val Lys Val Gln Ile Pro Gly
3160          835          840          845
3162 Leu Glu Asn Leu His Val Phe Val Pro Asp Ser Leu Ala Glu Glu Lys
3163          850          855          860
3165 Lys Ile Ile Leu Gln Leu Leu Asn Ala Ala Thr Gly Lys Asp Cys Ser
3166 865          870          875          880
3168 Lys Asp Pro Asp Asp Val Phe Met Asp Ala Phe Leu Leu Leu Thr Lys
3169          885          890          895

```

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Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\11262004\I608890.raw

```

3171 His Gly Asp Arg Ala Arg Asp Ser Glu Asp Gly Trp Gly Thr Trp Glu
3172          900          905          910
3174 Ala Arg Ala Val Lys Ile Val Pro Gln Val Glu Thr Val Asp Thr Leu
3175          915          920          925
3177 Arg Ser Met Gln Val Asp Asn Leu Leu Leu Val Val Met Glu Ser Ala
3178          930          935          940
3180 His Leu Val Leu Gln Arg Lys Ala Phe Gln Gln Ser Ile Glu Gly Leu
3181 945          950          955          960
3183 Met Thr Val Arg His Glu Gln Thr Ser Ser Gln Pro Ile Ile Ala Lys
3184          965          970          975
3186 Gly Leu Gln Gln Leu Lys Asn Asp Ala Leu Glu Leu Cys Asn Arg Ile
3187          980          985          990
3189 Ser Asp Ala Ile Asp Arg Val Asp His Met Phe Thr Leu Glu Phe Asp
3190          995          1000          1005
3192 Ala Glu Val Glu Glu Ser Glu Ser Ala Thr Leu Gln Gln Tyr Tyr Arg
3193 1010          1015          1020
3195 Glu Ala Met Ile Gln Gly Tyr Asn Phe Gly Phe Glu Tyr His Lys Glu
E--> 3196 1025/1025          1030          1035          1040
3198 Val Val Arg Leu Met Ser Gly Glu Phe Arg Gln Lys Ile Gly Asp Lys
3199          1045          1050          1055
3201 Tyr Ile Ser Phe Ala Gln Lys Trp Met Asn Tyr Val Leu Thr Lys Cys
3202          1060          1065          1070
3204 Glu Ser Gly Arg Gly Thr Arg Pro Arg Trp Ala Thr Gln Gly Phe Asp
3205          1075          1080          1085
3207 Phe Leu Gln Ala Ile Glu Pro Ala Phe Ile Ser Ala Leu Pro Glu Asp
3208 1090          1095          1100
3210 Asp Phe Leu Ser Leu Gln Ala Leu Met Asn Glu Cys Ile Gly His Val
E--> 3211 105/1105          1110          1115          1120
3213 Ile Gly Lys Pro His Ser Pro Val Thr Ala Ile His Arg Asn Ser Pro
3214          1125          1130          1135
3216 Arg Pro Val Lys Val Pro Arg Cys His Ser Asp Pro Pro Asn Pro His
3217          1140          1145          1150
3219 Leu Ile Ile Pro Thr Pro Glu Gly Phe Ser Thr Arg Ser Val Pro Ser
3220          1155          1160          1165
3222 Asp Ala Arg Thr His Gly Asn Ser Val Ala Ala Ala Ala Val Arg
3223          1170          1175          1180
3225 Ala Ala Ala Thr Thr Ala Ala Gly Arg Pro Gly Pro Gly Gly Gly Asp
E--> 3226 185/1185          1190          1195          1200
3228 Ser Val Pro Ala Lys Pro Val Asn Thr Ala Pro Asp Thr Arg Gly Ser
3229          1205          1210          1215
3231 Ser Val Pro Glu Asn Asp Arg Leu Ala Ser Ile Ala Ala Glu Leu Gln
3232          1220          1225          1230
3234 Phe Arg Ser Leu Ser Arg His Ser Ser Pro Thr Glu Glu Arg Asp Glu
3235          1235          1240          1245
3237 Pro Ala Tyr Pro Arg Ser Asp Ser Ser Gly Ser Thr Arg Arg Ser Trp
3238          1250          1255          1260
3240 Glu Leu Arg Thr Leu Ile Ser Gln Thr Lys Asp Ser Ala Ser Lys Gln
E--> 3241 265/1265          1270          1275          1280
3243 Gly Pro Ile Glu Ala Ile Gln Lys Ser Val Arg Leu Phe Glu Glu Arg

```

When numbering
the first
amino acid
on a line,
begin the
number directly
below the
first letter
of the amino
acid.

e.g. Glu |^S/_E| Ala
1025

same error on
page 5

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DATE: 11/26/2004

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Input Set : A:\pto.lm.txt

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```

3244          1285          1290          1295
3246 Arg Tyr Arg Glu Met Arg Arg Lys Asn Ile Ile Gly Gln Val Cys Asp
3247          1300          1305          1310
3249 Thr Pro Lys Ser Tyr Asp Asn Val Met His Val Gly Leu Arg Lys Val
3250          1315          1320          1325
3252 Thr Phe Lys Trp Gln Arg Gly Asn Lys Ile Gly Glu Gly Gln Tyr Gly
3253          1330          1335          1340
3255 Lys Val Tyr Thr Cys Ile Ser Val Asp Thr Gly Glu Leu Met Ala Met
E--> 3256 345          1350          1355          1360
3258 Lys Glu Ile Arg Phe Gln Pro Asn Asp His Lys Thr Ile Lys Glu Thr
3259          1365          1370          1375
3261 Ala Asp Glu Leu Lys Ile Phe Glu Gly Ile Lys His Pro Asn Leu Val
3262          1380          1385          1390
3264 Arg Tyr Phe Gly Val Glu Leu His Arg Glu Glu Met Tyr Ile Phe Met
3265          1395          1400          1405
3267 Glu Tyr Cys Asp Glu Gly Thr Leu Glu Glu Val Ser Arg Leu Gly Leu
3268          1410          1415          1420
3270 Gln Glu His Val Ile Arg Leu Tyr Thr Lys Gln Ile Thr Val Ala Ile
E--> 3271 425          1430          1435          1440
3273 Asn Val Leu His Glu His Gly Ile Val His Arg Asp Ile Lys Gly Ala
3274          1445          1450          1455
3276 Asn Ile Phe Leu Thr Ser Ser Gly Leu Ile Lys Leu Gly Asp Phe Gly
3277          1460          1465          1470
3279 Cys Ser Val Lys Leu Lys Asn Asn Ala Gln Thr Met Pro Gly Glu Val
3280          1475          1480          1485
3282 Asn Ser Thr Leu Gly Thr Ala Ala Tyr Met Ala Pro Glu Val Ile Thr
3283          1490          1495          1500
3285 Arg Ala Lys Gly Glu Gly His Gly Arg Ala Ala Asp Ile Trp Ser Leu
E--> 3286 505          1510          1515          1520
3288 Gly Cys Val Val Ile Glu Met Val Thr Gly Lys Arg Pro Trp His Glu
3289          1525          1530          1535
3291 Tyr Glu His Asn Phe Gln Ile Met Tyr Lys Val Gly Met Gly His Lys
3292          1540          1545          1550
3294 Pro Pro Ile Pro Glu Arg Leu Ser Pro Glu Gly Lys Ala Phe Leu Ser
3295          1555          1560          1565
3297 His Cys Leu Glu Ser Asp Pro Lys Ile Arg Trp Thr Ala Ser Gln Leu
3298          1570          1575          1580
3300 Leu Asp His Ala Phe Val Lys Val Cys Thr Asp Glu Glu
E--> 3301 585          1590          1595
3303 <210> SEQ ID NO: 15
3304 <211> LENGTH: 20 21 shown
3305 <212> TYPE: PRT
3306 <213> ORGANISM: synthetic construct
3308 <400> SEQUENCE: 15
3309 Ile Ile Gly Glu Val Cys Asp Thr Pro Lys Ser Tyr Asp Arg Val Met (16)
E--> 3310 1 5 10 15
3312 His Val Gly Leu Arg
E--> 3313 20 20 misaligned amino acid nos.
3315 <210> SEQ ID NO: 16

```

see item 10 on
Erra Summary
Sheet

invalid <213> response

delete

The <213> synthetic construct also appears in subsequent sequences.

Please correct them

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Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\11262004\I608890.raw

3316 <211> LENGTH: 14

3317 <212> TYPE: PRT

3318 <213> ORGANISM: synthetic construct

3320 <400> SEQUENCE: 16

E--> 3320 16

see p. 7 for explanation

09/608,890

7

<210> 16
<211> 14
<212> PRT
<213> synthetic construct

invalid

<400> 16

<220>

<223> Xaa at postions 3, 5, 6, 8, 10 and 11 = any amino acid

Ile Ser Xaa Pro Xaa Xaa Phe Xaa His Xaa Xaa His Val Gly
1 5 10

This goes below the (2207-2223) section, it goes directly above with the amino acids or nucleotides in a sequence

see p. 8 for more errors

09/608,890

8

from sequence 11.

ctg cag gag agc tgt gct gag ctg tgg acc agn gcc gac gac aac ggt 1109
Leu Gln Glu Ser Cys Ala Glu Leu Trp Thr Xaa Ala Asp Asp Asn Gly
110 115 120

"n" needs to be explained;

only the
Xaa was
explained
in the 12207-12237
section

FYI:

(see p. 9)

Per Sequence Rules, when explaining n's or Xaa's
in a sequence, use the 12207 through 12237
numeric identifiers. See 1.823 of Sequence Rules.

9

VARIABLE LOCATION SUMMARY

DATE: 11/26/2004

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TIME: 09:49:27

fyI

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\11262004\I608890.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:11; N Pos. 1094

Seq#:11; Xaa Pos. 116

Seq#:12; Xaa Pos. 116

Seq#:17; N Pos. 4,6,12,15

Seq#:18; N Pos. 3,6,9,12,18,20

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\11262004\I608890.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:1; Line(s) 24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43
Seq#:1; Line(s) 44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63
Seq#:1; Line(s) 64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83
Seq#:1; Line(s) 84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102
Seq#:1; Line(s) 103,104,105,106,107,108,109,110,111,112,113,114,115,116,117
Seq#:1; Line(s) 118,119,120,121,122,123,124,125,126,127,128,129,130,131,132
Seq#:1; Line(s) 133,134,135,136,137,138,139,140,141,142,143,144,145,146,147
Seq#:1; Line(s) 148,149,150,151,152,153,154,155,156,157,158,159,160,161,162
Seq#:1; Line(s) 163,164,165,166,167,168,169,170,171,172,173,174,175,176,177
Seq#:1; Line(s) 178,179,180,181,182,183,184,185,186,187,188,189,190,191,192
Seq#:1; Line(s) 193,194,195,196,197,198,199,200,201,202,203,204,205,206,207
Seq#:1; Line(s) 208,209,210,211,212,213,214,215,216,217,218,219,220,221,222
Seq#:1; Line(s) 223,224,225,226,227,228,229,230,231,232,233,234,235,236,237
Seq#:1; Line(s) 238,239,240,241,242,243,244,245,246,247,248,249,250,251,252
Seq#:1; Line(s) 253,254,255,256,257
Seq#:2; Line(s) 258,259,260,261,262,263,264,265,266,267,268,269,270,271,272
Seq#:2; Line(s) 273,274,275,276,277,278,279,280,281,282,283,284,285,286,287
Seq#:2; Line(s) 288,289,290,291,292,293,294,295,296,297,298,299,300,301,302
Seq#:2; Line(s) 303,304,305,306,307,308,309,310,311,312,313,314,315,316,317
Seq#:2; Line(s) 318,319,320,321,322,323,324,325,326,327,328,329,330,331,332
Seq#:2; Line(s) 333,334,335,336,337,338,339,340,341,342,343,344,345,346,347
Seq#:2; Line(s) 348,349,350,351,352,353,354,355,356,357,358,359,360,361,362
Seq#:2; Line(s) 363,364,365,366,367,368,369,370,371,372,373,374,375,376,377
Seq#:2; Line(s) 378,379,380,381,382,383,384,385,386,387,388,389,390
Seq#:3; Line(s) 391,392,393,394,395,396,397,398,399,400,401,402,403,404,405
Seq#:3; Line(s) 406,407,408,409,410,411,412,413,414,415,416,417,418,419,420
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RAW SEQUENCE LISTING ERROR SUMMARY
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Seq#:25; Line(s) 3429,3430
Seq#:26; Line(s) 3431,3432,3433,3434,3435,3436,3437,3438,3439,3440

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VERIFICATION SUMMARY

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Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\11262004\I608890.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
 L:2168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1061
 L:2169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1109
 L:2416 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:12
 L:2416 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:12
 L:2416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:112
 L:3196 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
 L:3211 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
 L:3226 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
 L:3241 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
 L:3256 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
 L:3271 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
 L:3286 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
 L:3301 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
 L:3310 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15
 L:3313 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15
 L:3313 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:5 SEQ:15
 L:3320 M:301 E: (44) No Sequence Data was Shown, SEQ ID:16
 L:3320 M:252 E: No. of Seq. differs, <211> LENGTH:Input:14 Found:0 SEQ:16
 L:3322 M:281 W: Numeric Fields not Ordered, <220> not ordered!.
 L:3323 M:281 W: Numeric Fields not Ordered, <223> not ordered!.
 L:3328 M:281 W: Numeric Fields not Ordered, <210> not ordered!.
 L:3340 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:17
 L:3340 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:17
 L:3340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
 L:3359 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:18
 L:3359 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:18
 L:3359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0